

## ASSESSING GENETIC DIVERSITY OF PAG SHEEP THROUGH PEDIGREE ANALYSES

Ramljak Jelena<sup>1\*</sup>, Špehar Marija<sup>2</sup>, Ivanković Ante<sup>1</sup>, Kasap Ante<sup>1</sup>

<sup>1</sup>University of Zagreb Faculty of Agriculture, Svetošimunska 25, 10000 Zagreb, Croatia

<sup>2</sup>Croatian Agency for Agriculture and Food, Svetošimunska 25, 10000 Zagreb, Croatia

\*Corresponding author: [jramljak@agr.hr](mailto:jramljak@agr.hr)

**ABSTRACT:** Changes in agricultural production systems over the past 50 years have led to erosion of animal genetic resources worldwide. One of the most affected species are autochthonous breeds, which play an important role in livelihoods due to their low-input production systems and good adaptation to environmental changes. Therefore, it is important to characterize and monitor their population structure in order to conserve the genetic variability. There are several approaches to analyse genetic structure, but one of the cheapest and most common is pedigree analysis. The aim of this study was to highlight an in-depth analysis of the pedigree of Croatian autochthonous breed - Pag sheep, in order to investigate the structure, inbreeding level and other parameters of genetic variability. Data was provided by the Croatian Ministry of Agriculture and included 10,380 animals (total population) of which 3,701 born between 2011 and 2018 were used as reference population. The reference population was the basis for analysis of studied population parameters with an exception of some parameters of pedigree quality. Pedigree analysis was performed using ENDOG v 4.8 software and POPREP software system that provides comprehensive reports for population management. In the total population, the maximum number of traced generation was nine and the number of fully traced generation was four. In the reference population, the pedigree completeness was 89.8% in the first parenteral generation and declined with increasing the depth of pedigree to 22% in the fourth generation. The average equivalent complete generations, as a measure of pedigree completeness, was 2.3. The average generation interval was  $4.9 \pm 2.5$  years, with ewes being used for longer periods than rams. Intervals ranged from  $3.8 \pm 1.5$  (sire pathway) to  $5.9 \pm 2.8$  years (dam pathway). Genealogical parameters estimated based on probabilities of gene origin, including equivalent number of founders ( $f_{eq}$ ) and ancestors ( $f_{ea}$ ), effective number of founders ( $f_e$ ) and ancestors ( $f_a$ ) were estimated at 1,952, 1,969, 452, and 333, respectively. The  $f_e/f_a$  ratio was 1.36 and may indicate reduction of genetic variability. The number of founders was 2,108, while the 141 most influential ancestors explained 50% of the total genetic variations in the reference population. The average inbreeding coefficient in the reference population was 1.0%, with inbreeding rate per generation ( $\Delta F$ ) of 0.6%. The proportion of inbred animals from the reference population was 3.9% (145 animals) with the average inbreeding coefficient of 16.47%. The majority of inbred animals (55%) had an inbreeding coefficient in the range from 10 to 15%. Only 2.1% individuals had an inbreeding coefficients greater than 25%. The estimated genetic population parameters indicate satisfactory level of genetic variability in the Pag sheep breed. However, recent inbreeding rate calls for more attention in future breeding plans to slow down the inevitable loss of genetic variability in this population under selection on dairy traits.

**Keywords:** sheep, pedigree, genetic diversity, inbreeding

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